

**Figure 1:**

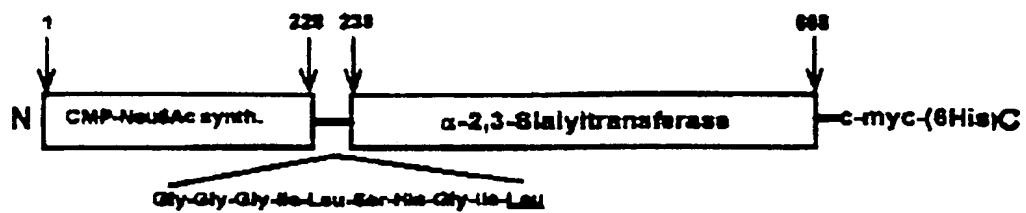
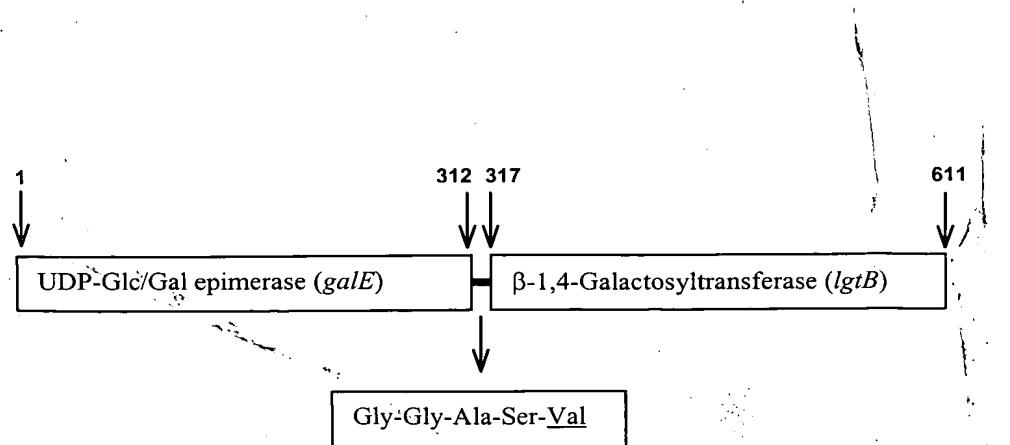


Figure 2

ATGCAAAACCACGTTATCAGCTTAGCTTCCGCCGCAGAACGCAGGGCGCACATTGCCGAT  
 1 TACGTTTGGTGAATAGTCAAATCGAAGGCGGCGTCTTGCGTCCCGCGTGTAAACGGCTA 60  
     M Q N H V I S L A S A A E R R A H I A D -  
  
 ACCTTCGGCAGGCACGGCATCCCGTTCAGTTTGCAGCAGCACTGATGCCGCTTGAAAGG  
 61 TGGAAAGCCGTCGGCTAGGGCAAAGTCAAAAAGCTCGGTGACTACGGCAGACTTCC 120  
     T F G R H G I P F Q F F D A L M P S E R -  
  
 CTGGAACAGGCAATGGCGGAACCGTCCCCGGTTGCGCGCACCCCTATTGAGCGGA  
 121 GACCTTGTCCGTTACCGCCTTGAGCAGGGCGAACAGCCGCGTGGGATAAAACTCGCCT 180  
     L E Q A M A E L V P G L S A H P Y L S G -  
  
 GTGGAAAAAGCCTGTTATGAGCCACGCCGTATTGAGGAAAGCAGGCATTGGACGAAGGT  
 181 CACCTTTTCGGACGAAATACTCGGTGCGGCATAACACCTTCGTCGTAACCTGCTTCCA 240  
     V E K A C F M S H A V L W K Q A L D E G -  
  
 CTGCCGTATATCACCGTATTGAGGACGACGTTTACTCGCGAACGGTGAGGAAAAATTG  
 241 GACGGCATATACTGGCATAAAACCTCTGCTGCAAAATGAGCCGCTTCACTCCTTTAAG 300  
     L P Y I T V F E D D V L L G E G E E K F -  
  
 CTTGCCGAAGACGCTTGGCTGCAAGAACGCTTGACCCGGATACGCCCTTATCGTCCGC  
 301 GAACGGCTTCTGCGAACCGACGTTCTGCGAAACTGGGCCTATGGCGGAATAGCAGGGC 360  
     L A E D A W L Q E R F D P D T A F I V R -  
  
 TTGGAAACGATGTTATGCACGTCTGACCTCGCCCTCCGGTGGCGGATTACTGCGGG  
 361 AACCTTTGCTACAAATACTGCACTGGAGACTGGAGCGGGAGGCCGACCGCCTAATGACGCC 420  
     L E T M F M H V L T S P S G V A D Y C G -  
  
 CGGCCCTTCCGCTGTTGGAAAGCGAACACTGGGGACGGCGGCTATATCATTCCCGA  
 421 GCGCGAAAGGCACAACCTTCGCTTGACCCCCCTGCCGCCGATATAGTAAAGGGCT 480  
     R A F P L L E S E H W G T A G Y I I S R -  
  
 AAAGCGATGCGGTTTCTGGACAGGTTGCGCCCTGCCGCCGAAGGGCTGCACCCC  
 481 TTTCGCTACGCAAAGGACTGTCAAACGGCGGACGGCGGCTCCGACGTGGGG 540  
     K A M R F F L D R F A A L P P E G L H P -  
  
 GTCGATCTGATGATGTTACCGATTTTCGACAGGGAAGGAATGCCGTTGCCAGCTC  
 541 CAGCTAGACTACTACAAGTCGCTAAAAAGCTGTCCCAAACGGCGGACGGCGGCTCCGACGTGGGG 600  
     V D L M M F S D F F D R E G M P V C Q L -  
  
 AATCCCGCCTTGTGCCAACAGAGCTGCATTATGCCAAGTTTACGACCAAAACAGCGCA  
 601 TTAGGGCGGAACACGCCGGTTCTGACGTAATACGGTCAAAGTGTGGTTTGTCGCGT 660  
     N P A L C A Q E L H Y A K F H D Q N S A -  
  
 TTGGGCAGCCTGATCGAACACGCCGCTCTGAACCGAACAGCAAAGGGCGGATTCC  
 661 AACCCGTCGGACTAGTTGTGCTGGCGGAGGACTTGGCGTTGTGCTTCCGCGCTAAGG 720  
     L G S L I E H D R L L N R K Q Q R R D S -  
  
 CCCGCCAACACATTCAAACACCGCCTGATCCGCGCCTTGACCAAAATCAGCAGGGAAAGG  
 721 GGGCGGTTGTGTAAGTTGTGCGGACTAGGCGCGAACCTGGTTTAGTCGCTCCCTTCC 780  
     P A N T F K H R L I R A L T K I S R E R -  
  
 GAAAAACGCCGCAAAGCGCGAACAGTCATTGTGCCCTTCCAATAA  
 781 CTTTTTGCAGGCCGTTCCGCGCTTGTCAAGTAACACGGAAAGGTTATT 828  
     E K R R Q R R E Q F I V P F Q \* -

**Figure 3**



**Figure 4**

- A. 5' primer for amplification of *galE* for insertion into pCW at the BamHI site

5' GGACAGGATCCATCGATGCTAGGAGGTATGGCAATTAGTATTAGGTGGAGC 3'  
BamHI Met

- B. 3' primer for amplification of *galE* for fusion with *lgtB* insertion into pCW**

5' GGGGGGG**G****T****A****G****C****G****C****G****C****T****C****C****T****G****A****T****C****G****T****A****C****C****T****T****T****G** 3'  
          **NheI**   **Gly**   **Gly**

- C. 5' primer for amplification of *lgtB* for fusion with the 3' end of *galE*.

5' GGGGGG**GCTAGCGTGCAAAAC**ACGTTATCAGCTTAGC  
            **NheI**    **Val**

- D. 3' primer for amplification of *lgtB* for fusion with *galE* and insertion into pCW

5' GGGGGGG**T****C****G****A****C****T****A****T****T****G****G****A****A****G****G****C****A****C****A****A****T****G****A****A****C****T****G****T****C****G****C****G**  
Sall

- ## E. Junction region of the *galE-lgtB* fusion

*gale* NheI *lgtB*  
 5' CCA AAA GGG TAC GAT GAT CGA GGA GGC GGA **GCT AGC** GTG CAA AAC CAC GTT ATC AGC TTA GCT 3'  
 3' GGT TTT CCC ATG CTA CTA GCT CCT CCG CCT **CGA TCG** CAC GTT TTG GTG CAA TAG TCG AAT CGA 5'  
 P K G Y D R G G G A S V O N H V I S L A